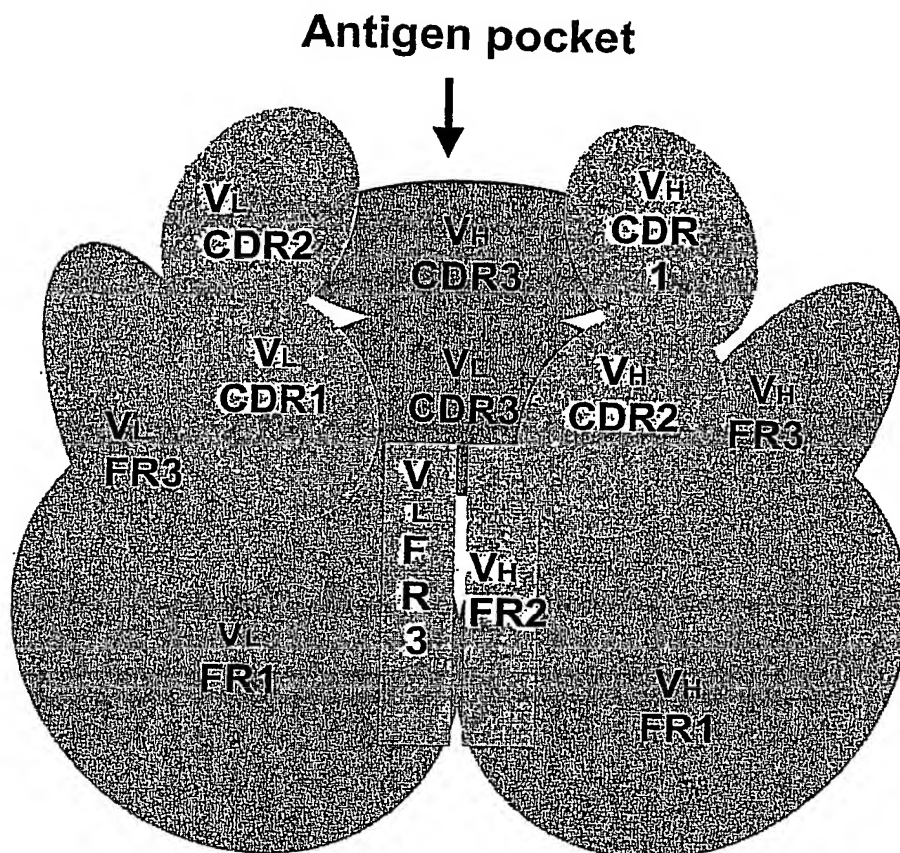


1/19

Fig. 1

Fa



CDR: complementarity determining region

FR: frame region

V<sub>L</sub>: variable light chain

V<sub>H</sub>: variable heavy chain

BEST AVAILABLE COPY

2/19

Fig. 2a

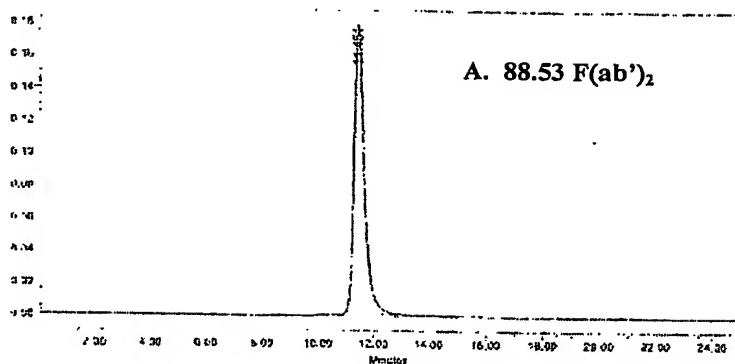


Fig. 2b

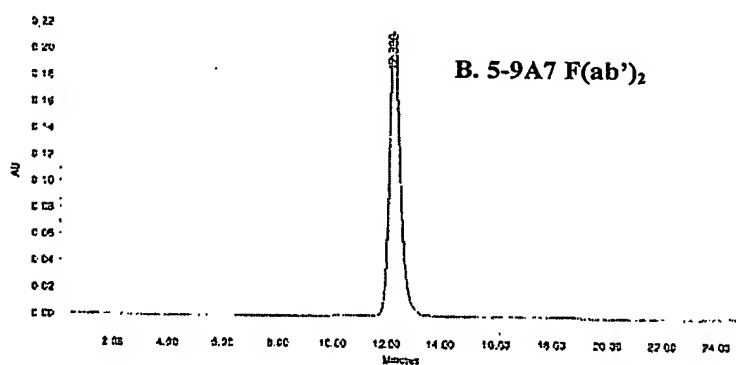
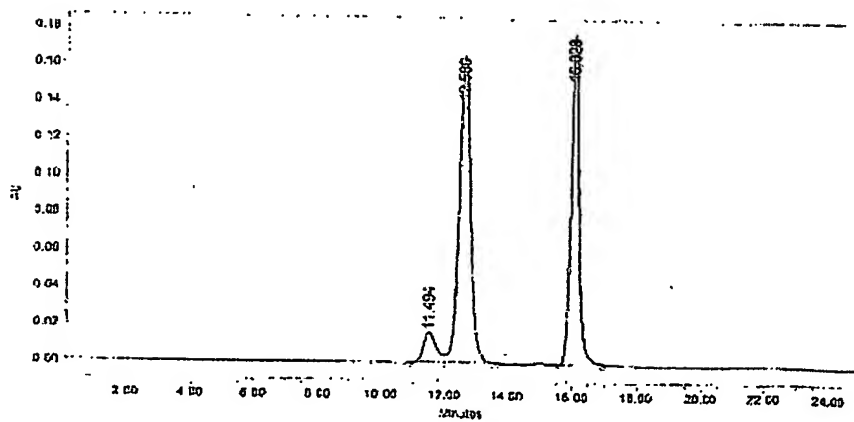


Fig. 3



3/19

Fig. 4

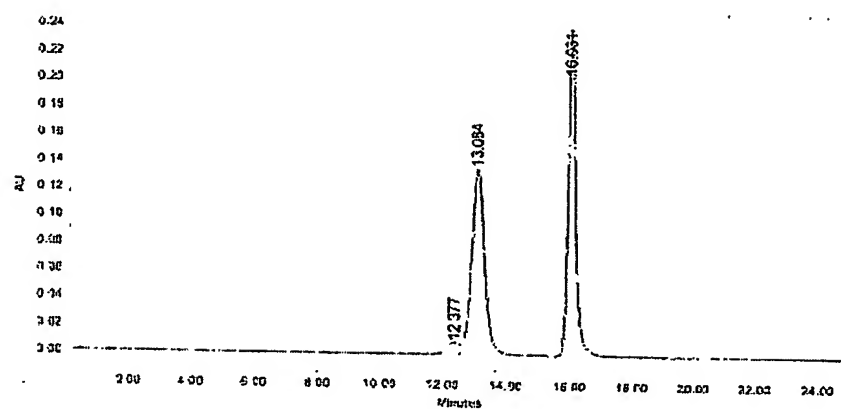


Fig. 5

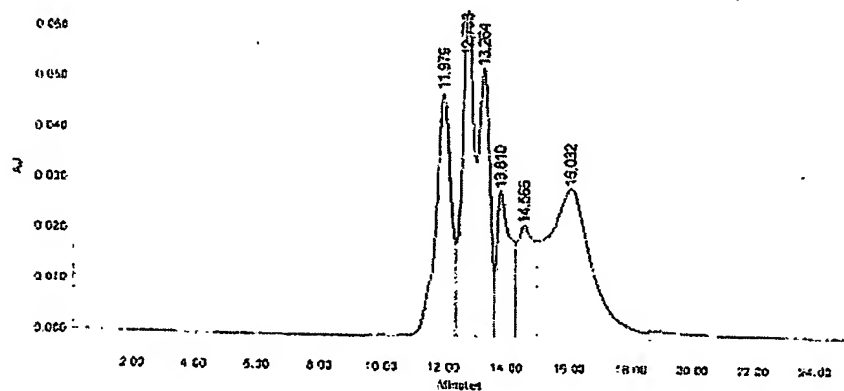
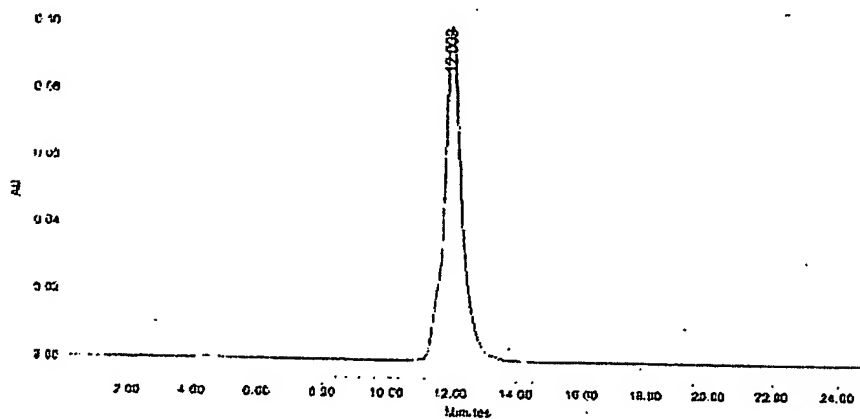


Fig. 6



4/19

Fig. 7a

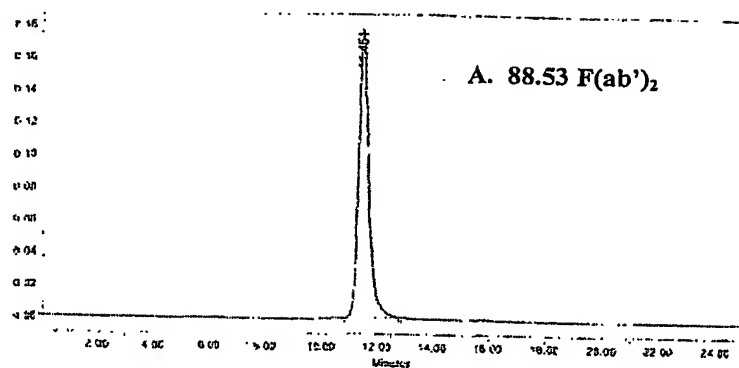


Fig. 7b

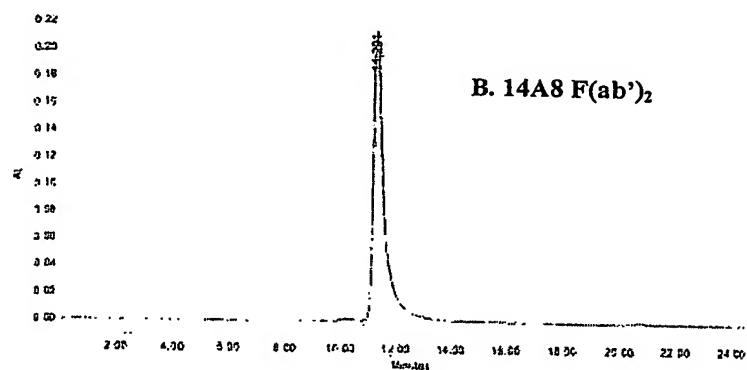
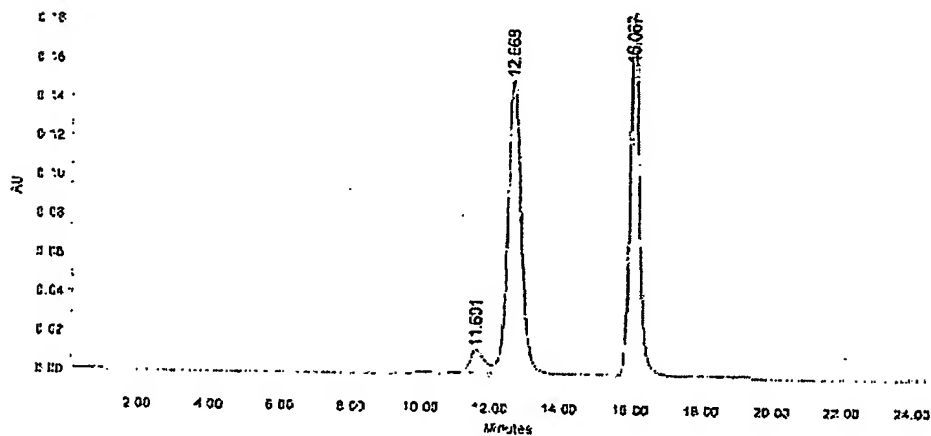


Fig. 8



5/19

Fig. 9

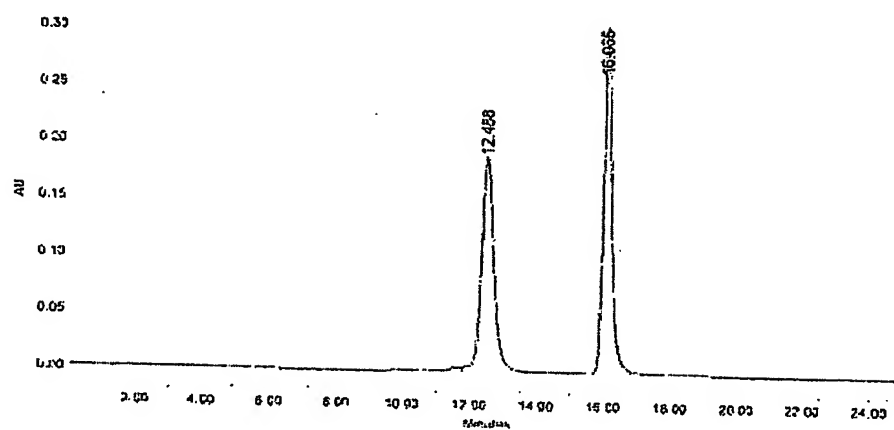


Fig. 10

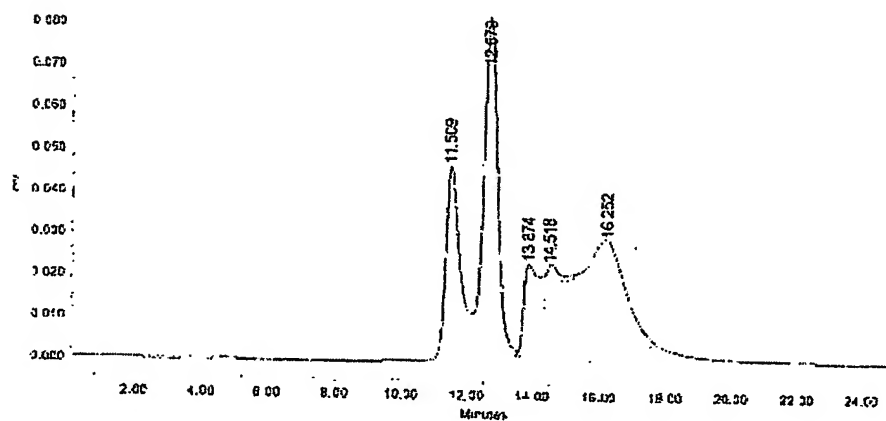


Fig. 11

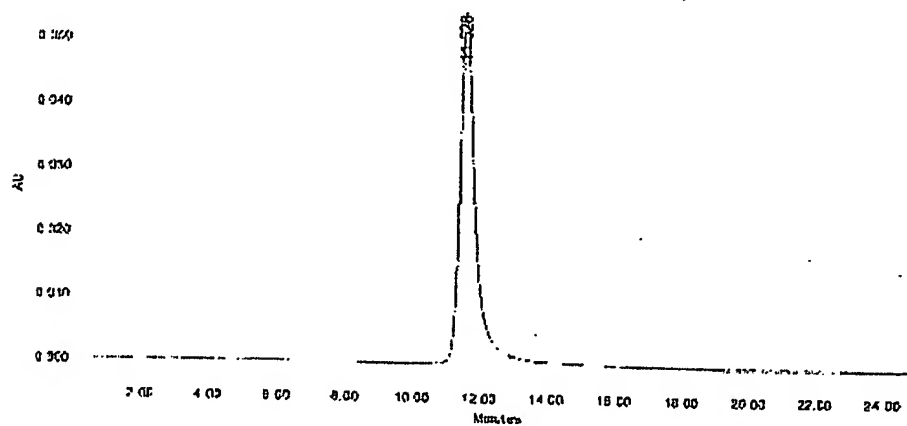
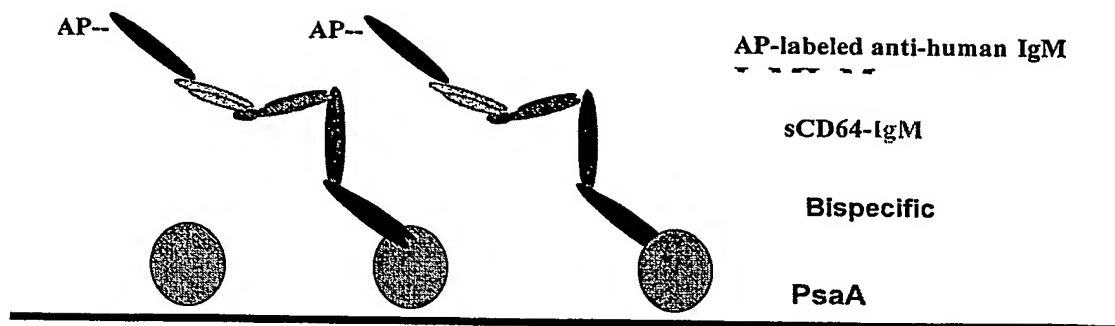


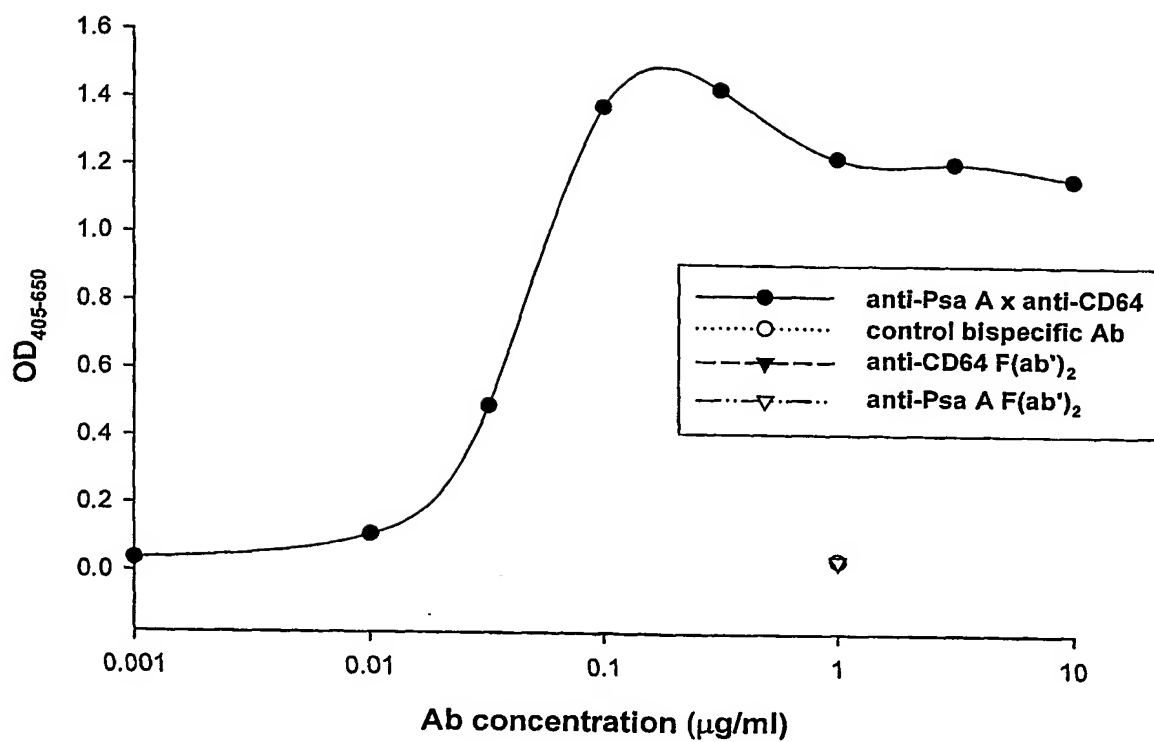
Fig. 12

6/19



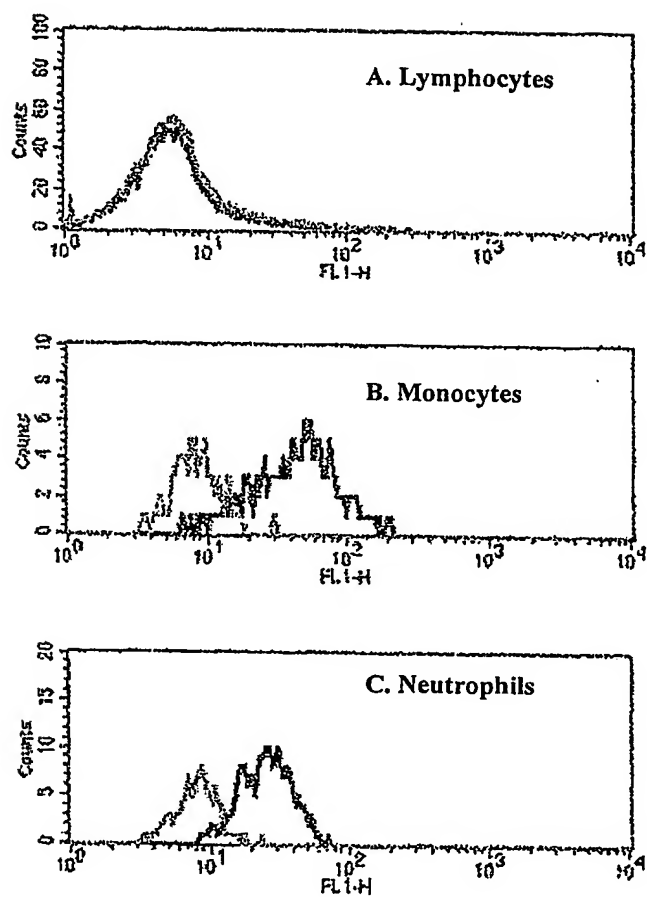
7/19

Fig. 13



8/19

Fig. 14





9/19

Fig. 15

1	ATG AAA AAA TTA GGT ACA TTA CTC GTT CTC TTT CTT TCT GCA ATC	45
1	Met Lys Lys Leu Gly Thr Leu Leu Val Leu Phe Leu Ser Ala Ile	15
46	ATT CTT GTA GCA TGT GCT AGC GGA AAA AAA GAT ACA ACT TCT GGT	90
16	Ile Leu Val Ala Cys Ala Ser Gly Lys Lys Asp Thr Thr Ser Gly	30
91	CAA AAA CTA AAA GTT GTT GCT ACA AAC TCA ATC ATC GCT GAT ATT	135
31	Gln Lys Leu Lys Val Val Ala Thr Asn Ser Ile Ile Ala Asp Ile	45
136	ACT AAA AAT ATT GCT GGT GAC AAA ATT GAC CTT CAT AGT ATC GTT	180
46	Thr Lys Asn Ile Ala Gly Asp Lys Ile Asp Leu His Ser Ile Val	60
181	CCG ATT GGG CAA GAC CCA CAC GAA TAC GAA CCA CTT CCT GAA GAC	225
61	Pro Ile Gly Gln Asp Pro His Glu Tyr Glu Pro Leu Pro Glu Asp	75
226	GTT AAG AAA ACT TCT GAG GCT GAT TTG ATT TTC TAT AAC GGT ATC	270
76	Val Lys Lys Thr Ser Glu Ala Asp Leu Ile Phe Tyr Asn Gly Ile	90
271	AAC CTT GAA ACA GGT GGC AAT GCT TGG TTT ACA AAA TTG GTA GAA	315
91	Asn Leu Glu Thr Gly Gly Asn Ala Trp Phe Thr Lys Leu Val Glu	105
316	AAT GCC AAG AAA ACT GAA AAC AAA GAC TAC TTC GCA GTC AGC GAC	360
106	Asn Ala Lys Lys Thr Glu Asn Lys Asp Tyr Phe Ala Val Ser Asp	120
361	GGC GTT GAT GTT ATC TAC CTT GAA GGT CAA AAT GAA AAA GGA AAA	405
121	Gly Val Asp Val Ile Tyr Leu Glu Gly Gln Asn Glu Lys Gly Lys	135
406	GAA GAC CCA CAC GCT TGG CTT AAC CTT GAA AAC GGT ATT ATT TTT	450
136	Glu Asp Pro His Ala Trp Leu Asn Leu Glu Asn Gly Ile Ile Phe	150
451	GCT AAA AAT ATC GCC AAA CAA TTG AGC GCC AAA GAC CCT AAC AAT	495
151	Ala Lys Asn Ile Ala Lys Gln Leu Ser Ala Lys Asp Pro Asn Asn	165
496	AAA GAA TTC TAT GAA AAA AAT CTC AAA GAA TAT ACT GAT AAG TTA	540
166	Lys Glu Phe Tyr Glu Lys Asn Leu Lys Glu Tyr Thr Asp Lys Leu	180
541	GAC AAA CTT GAT AAA GAA AGT AAG GAT AAA TTT AAT AAG ATC CCT	585
181	Asp Lys Leu Asp Lys Glu Ser Lys Asp Lys Phe Asn Lys Ile Pro	195
586	GCT GAA AAG AAA CTC ATT GTA ACC AGC GAA GGA GCA TTC AAA TAC	630
196	Ala Glu Lys Lys Leu Ile Val Thr Ser Glu Gly Ala Phe Lys Tyr	210
631	TTC TCT AAA GCC TAT GGT GTT CCA AGT GCC TAC ATC TGG GAA ATC	675
211	Phe Ser Lys Ala Tyr Gly Val Pro Ser Ala Tyr Ile Trp Glu Ile	225
676	AAT ACT GAA GAA GAA GGA ACT CCT GAA CAA ATC AAG ACC TTG GTT	720
226	Asn Thr Glu Glu Glu Gly Thr Pro Glu Gln Ile Lys Thr Leu Val	240
721	GAA AAA CTT CGC CAA ACA AAA GTT CCA TCA CTC TTT GTA GAA TCA	765
241	Glu Lys Leu Arg Gln Thr Lys Val Pro Ser Leu Phe Val Glu Ser	255
766	AGT GTG GAT GAC CGT CCA ATG AAA ACT GTT TCT CAA GAC ACA AAC	810
256	Ser Val Asp Asp Arg Pro Met Lys Thr Val Ser Gln Asp Thr Asn	270
811	ATC CCA ATC TAC GCA CAA ATC TTT ACT GAC TCT ATC GCA GAA CAA	855
271	Ile Pro Ile Tyr Ala Gln Ile Phe Thr Asp Ser Ile Ala Glu Gln	285
856	GGT AAA GAA GGC GAC AGC TAC TAC AGC ATG ATG AAA TAC AAC CTT	900
286	Gly Lys Glu Gly Asp Ser Tyr Tyr Ser Met Met Lys Tyr Asn Leu	300
901	GAC AAG ATT GCT GAA GGA TTG GCA AAA TAA	930
301	Asp Lys Ile Ala Glu Gly Leu Ala Lys End	

10/19

Fig. 16a

```

      D   I   Q   M   T   Q   S   P   S   S   L   S   A   S   V   G   D   R
1    GAC ATC CAG ATG ACC CAG TCT CCA TCC TCA CTG TCT GCA TCT GTA GGA GAC AGA

                                CDR1
      V   T   I   T   C   R   A   S   Q   G   I   S   S   W   L   A   W   Y
55   GTC ACC ATC ACT TGT CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC TGG TAT

                                CDR2
      Q   Q   K   P   E   K   A   P   E   S   L   I   Y   V   A   S   S   L
109  CAG CAG AAA CCA GAG AAA GCC CCT GAG TCC CTG ATC TAT GTT GCA TCC AGT TTG

      CDR2
      ~~~~~
      Q   S   G   V   P   S   R   F   S   G   S   G   S   G   T   D   F   T
163  CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAT TTC ACT

                                CDR3
      L   T   I   S   S   L   Q   P   E   D   F   A   T   Y   Y   C   Q   Q
217  CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT TAT TAC TGC CAA CAG

      CDR3
      ~~~~~
      Y   N   S   Y   P   P   T   F   G   Q   G   T   K   V   E   I   K
271  TAT AAT AGC TAT CCT CCG ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA

      ↳ JK1

```

Fig. 16b

```

      Q   V   R   L   Q   Q   W   G   A   G   L   L   K   P   S   E   T   L
1    CAG GTG CGA CTA CAG CAG TGG GGC GCA GGA CTG TTG AAG CCT TCG GAG ACC CTG

                                CDR1
      S   L   T   C   A   V   F   G   G   S   F   S   G   F   S   W   S   W
55   TCC CTC ACC TGC GCT GTC TTT GGT GGG TCC TTC AGT GGT TTC TCC TGG AGC TGG

                                CDR2
      I   R   Q   T   P   G   K   G   L   E   W   I   G   E   I   D   Y   R
109  ATC CGC CAG ACC CCA GGG AAG GGG CTG GAG TGG ATC GGG GAA ATC GAT TAT AGA

      CDR2
      ~~~~~
      G   S   T   N   Y   N   P   S   L   K   S   R   V   T   I   L   R   D
163  GGA AGC ACC AAC TAC AAC CCG TCC CTC AAG AGT CGA GTC ACC ATA TTA AGA GAC

      T   S   R   S   Q   F   S   L   K   L   S   S   V   T   A   A   D   S
217  ACG TCC AGG AGC CAG TTC TCC CTG AAG TTG AGC TCC GTG ACC GCC GCG GAC TCG

```

11/19

```

      A   V   F   Y   C   A   R   G   G   P   R   F   D   Y   W   G   Q   G
271  GCT GTG TTT TAT TGT GCG AGA GGG GGG CCC CGC TTT GAC TAC TGG GGC CAG GGA
      L       JH4b
      T   L   V   T   V   S   S
325  ACC CTG GTC ACC GTC TCC TCA

```

Fig. 17a

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E   R
1   GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA

      CDR1
      A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A   W   Y
55  GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCN TGG TAC

      CDR2
      Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A   S   N   R
109 CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA TCC AAC AGG

      CDR2
      A   T   G   I   P   A   R   F   S   G   S   G   S   G   T   D   F   T
163 GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT

      CDR3
      L   T   I   S   S   L   E   P   E   D   F   A   V   Y   Y   C   Q   Q
217 CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT TAT TAC TGT CAG CAG

      CDR3
      R   S   N   W   P   L   T   F   G   G   G   T   K   V   E   I   K
271 CGT AGC AAC TGG CCT CTC ACT TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA

```

Fig. 17b

```

      E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G   S   L
1   GAG GTG CAA CTA GTG GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG TCC CTG

      CDR1
      R   L   S   C   A   A   S   G   F   T   F   N   I   F   G   M   S   W
55  AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AAT ATC TTT GGG ATG AGC TGG

      CDR2
      V   R   Q   A   P   G   K   G   L   E   W   V   A   N   I   K   Q   D
109 GTC CGC CAG GCT CCA GGG AAA GGG CTG GAG TGG GTG GCC AAC ATA AAG CAA GAT

```

12/19

CDR2

~~~~~

163    G   S   E   K   Y   Y   V   D   S   V   K   G   R   F   T   I   S   R  
       GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG AAG GGC CGA TTC ACC ATC TCC AGA

217    D   N   A   K   N   S   L   Y   L   Q   M   N   S   L   R   A   E   D  
       GAC AAC GCC AAG AAC TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC

CDR3

~~~~~

271    T   A   V   Y   Y   C   A   R   D   R   F   Y   Y   G   S   G   S   Y  
       ACG GCT GTG TAT TAC TGT GCG AGG GAT CGG TTT TAC TAT GGT TCG GGG AGT TAT

└─ JH6b

CDR3

~~~~~

325    Y   Y   Y   Y   N   G   M   D   V   W   G   Q   G   T   T   V   T   V  
       TAT TAC TAC TAC AAC GGT ATG GAC GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC

379    S   S  
       TCC TCA

Fig. 18a

1    E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E   R  
       GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA

CDR1

~~~~~

55    A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A   W   Y  
       GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC TGG TAC

CDR2

~~~~~

109    Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A   S   N   R  
       CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA TCC AAC AGG

CDR2

~~~~~

163    A   T   G   I   P   A   R   F   S   G   S   G   S   G   T   D   F   T  
       GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT

CDR3

~~~~~

217    L   T   I   S   S   L   E   P   E   D   F   A   V   Y   Y   C   Q   Q  
       CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT TAT TAC TGT CAG CAG

CDR3

~~~~~

271    R   S   N   W   P   P   F   T   F   G   P   G   T   K   V   D   I   K  
       CGT AGC AAC TGG CCT CCA TTC ACT TTC GGC CCT GGG ACC AAA GTG GAT ATC AAA

└─ JK3

13/19

Fig. 18b

```

      E  V  Q  L  V  E  S  G  G  G  L  V  Q  P  G  G  S  L
1    GAG GTA CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC CAG CCG GGG GGG TCC CTG

                                     CDR1
                                     ~~~~~
      R  L  S  C  A  A  S  G  F  T  F  S  S  F  W  M  S  W
55   AGA CTC TCC TGT GCA GCT TCT GGA TTC ACC TTT AGT AGC TTT TGG ATG AGC TGG

                                     CDR2
                                     ~~~~~
      V  R  Q  A  P  G  K  G  L  E  W  V  A  N  I  K  Q  D
109  GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA AAG CAA GAT

      CDR2
      ~~~~~
      G  S  E  K  F  Y  V  D  S  V  K  G  R  F  T  I  S  R
163  GGA AGT GAG AAA TTC TAT GTG GAC TCT GTG AAG GGC CGA TTC ACC ATC TCC AGA

      D  N  A  K  N  S  L  Y  L  Q  M  N  S  L  R  A  E  D
217  GAC AAC GCC AAG AAC TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC

                                     CDR3
                                     ~~~~~
      T  A  V  Y  Y  C  A  R  D  R  I  T  M  V  R  P  Y  Y
271  ACG GCT GTG TAT TAC TGT GCG AGG GAT CGT ATT ACA ATG GTT CGG CCC TAT TAC

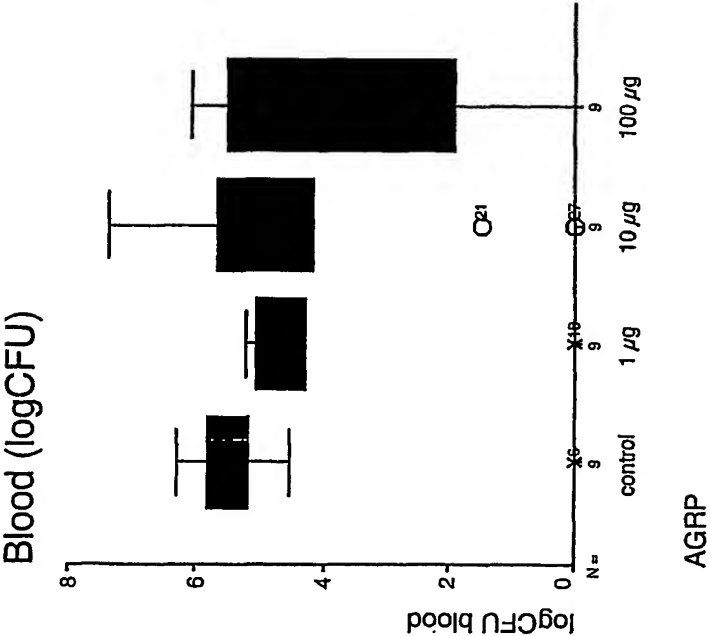
      CDR3
      ~~~~~
                                     JH6b
                                     ~~~~~
      Y  F  Y  N  G  L  D  V  W  G  Q  G  T  T  V  T  V  S
325  TAC TTC TAC AAC GGT CTG GAC GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC

      S
379  TCA

```

Figure 19A

9A7

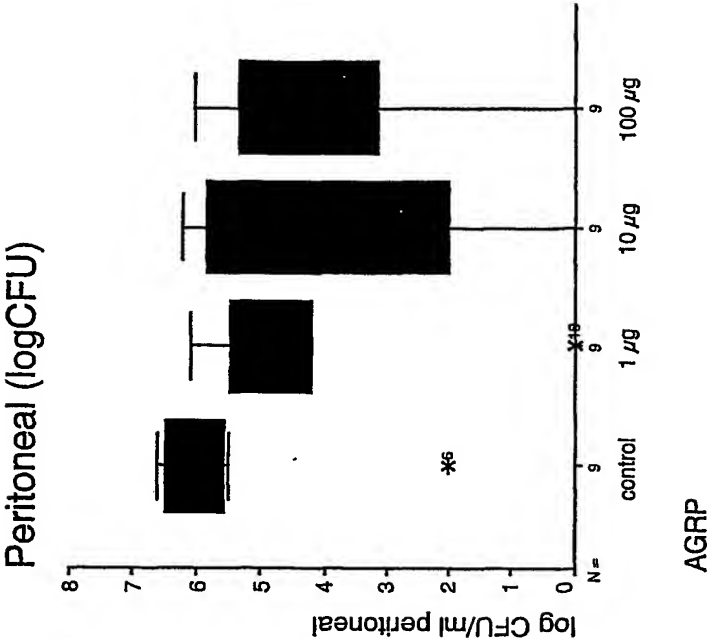


Test Statistics<sup>a,b</sup>

	CFU/ml blood
Chi-Square	4,711
df	3
Asymp. Sig.	,194

a. Kruskal Wallis Test  
b. Grouping Variable: AGRP

14/19



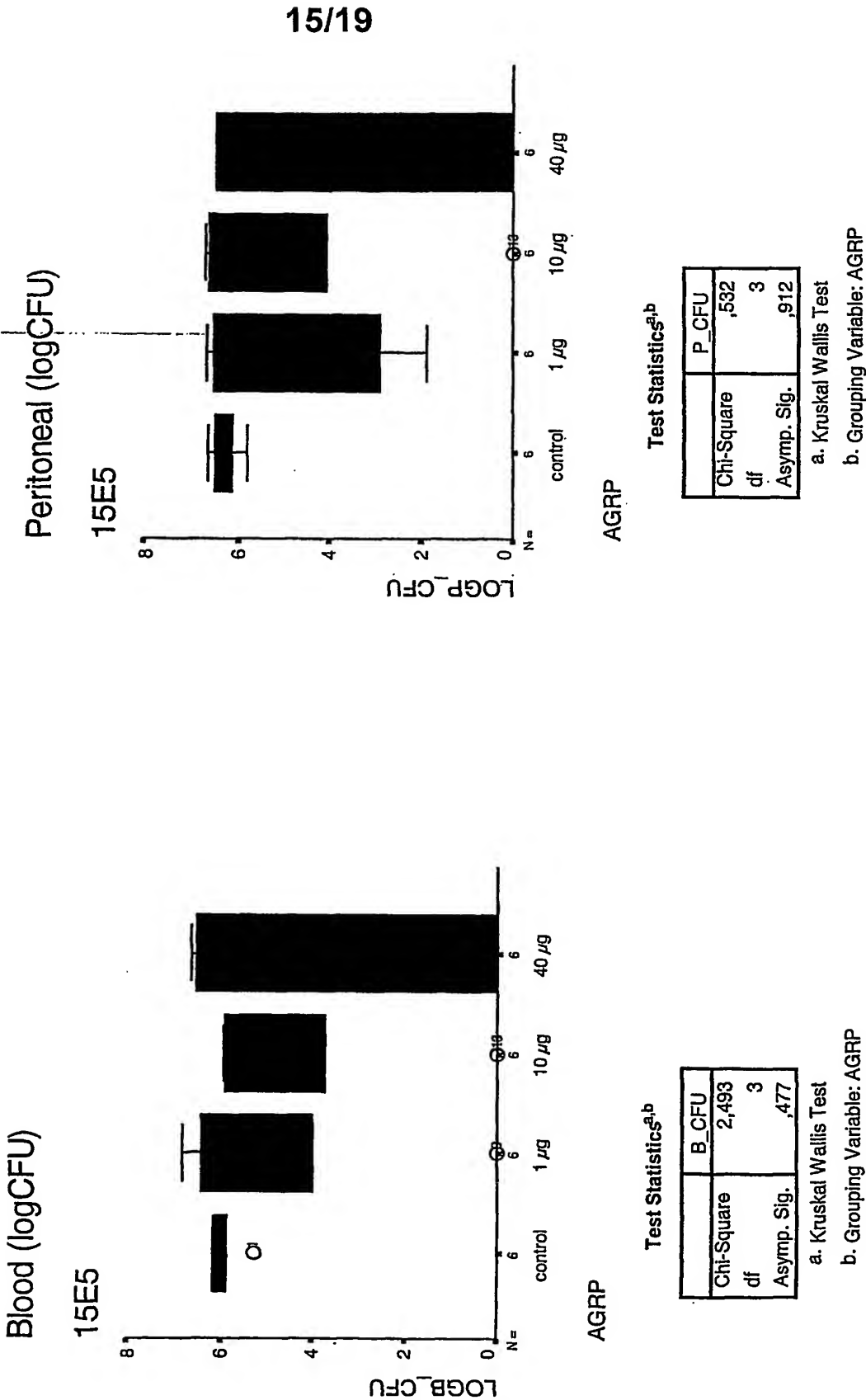
Test Statistics<sup>a,b</sup>

	CFU/ml peritoneal
Chi-Square	7,926
df	3
Asymp. Sig.	,048

a. Kruskal Wallis Test  
b. Grouping Variable: AGRP

15E5

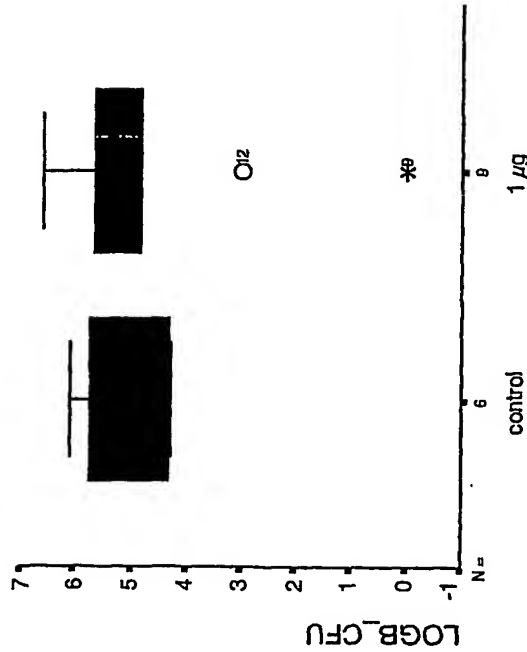
Figure 19B



1G9

Blood (log CFU)

1G9.1



Ab

Test Statistics<sup>b</sup>

	B_CFU
Mann-Whitney U	23,000
Wilcoxon W	44,000
Z	-,471
Asymp. Sig. (2-tailed)	,637
Exact Sig. [2*(1-tailed Sig.)]	,689 <sup>a</sup>

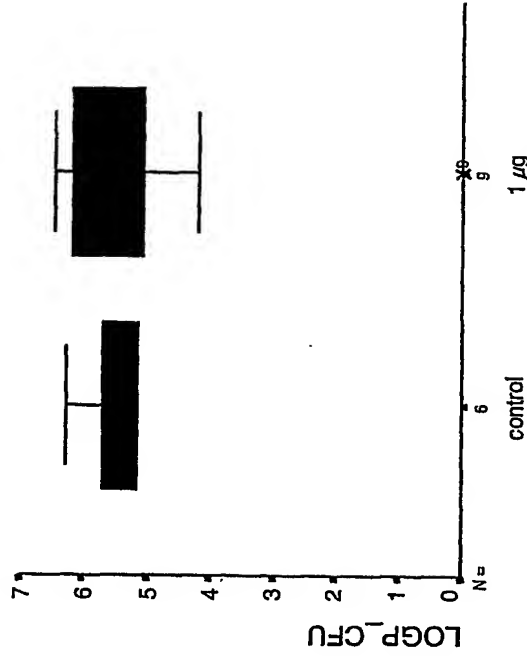
a. Not corrected for ties.

b. Grouping Variable: AGRP

Figure 19C

Peritoneal (log CFU)

1G9.1



Ab

Test Statistics<sup>b</sup>

	P_CFU
Mann-Whitney U	22,500
Wilcoxon W	43,500
Z	-,531
Asymp. Sig. (2-tailed)	,596
Exact Sig. [2*(1-tailed Sig.)]	,607 <sup>a</sup>

a. Not corrected for ties.

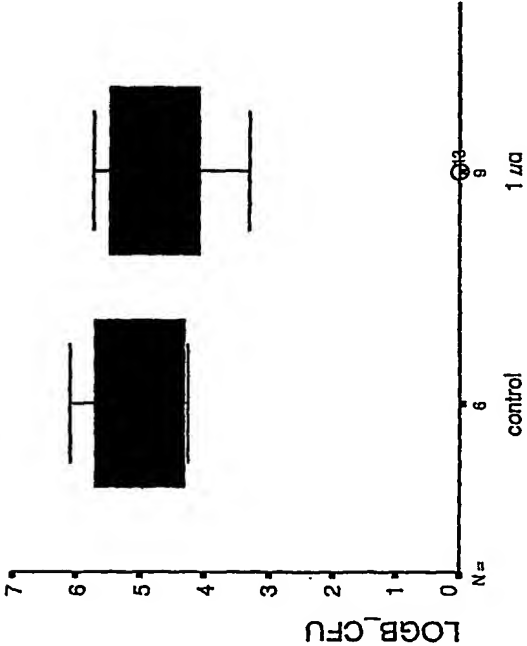
b. Grouping Variable: AGRP



3D10

Blood (log CFU)

3D10



Test Statistics<sup>b</sup>

	B_CFU
Mann-Whitney U	23,000
Wilcoxon W	68,000
Z	-.471
Asymp. Sig. (2-tailed)	.637
Exact Sig. [2*(1-tailed Sig.)]	.689 <sup>a</sup>

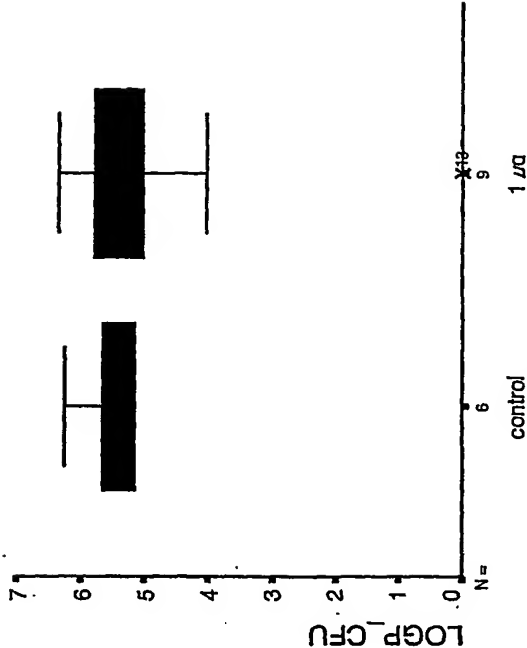
a. Not corrected for ties.

b. Grouping Variable: AGRP

Figure 19D

Peritoneal (log CFU)

3D10



Test Statistics<sup>b</sup>

	P_CFU
Mann-Whitney U	27,000
Wilcoxon W	72,000
Z	.000
Asymp. Sig. (2-tailed)	1,000
Exact Sig. [2*(1-tailed Sig.)]	1,000 <sup>a</sup>

a. Not corrected for ties.

b. Grouping Variable: AGRP



19/19

Fig. 20

Clone	Sub type	c1q	R6 ELISA (corrected)			R6 WB 2 µg/ml	ELISA (0.5 µg/ml) (corrected)										Western Blot (2 µg/ml)											
			5 µg/ml	0.5 µg/ml	50 ng/ml		5 ng/ml	R6	1	3	4	6B	7F	8	9V	12F	14	23F	D39	R6	1	3	4	6B	7F	8	9V	12F
1-7D12	G3		1.58	0.35	0.23	0.20	0.20	0	0.42	0.45	0.38	0.40	0.60	0.49	0.55	0.44	0.51	0.38	0.40	1.23	0	0	0	0	0	0	0	0
1-7H7	G3		0.00	0.50	0.22	0.19	0.20	0	0.38	0.52	0.40	0.49	0.64	0.53	0.62	0.50	0.60	0.39	0.44	0.69	0	0	0	0	0	0	0	0
1-11H10	G3		0.00	0.86	0.52	0.26	0.22	1	0.90	0.30	0.79	0.26	0.39	0.81	1.08	2.56	1.10	0.77	0.24	0.06	1	1	1	1	1	1	1	1
1-12E10	G3		2.01	0.42	0.24	0.21	0.21	0	0.56	0.47	0.29	0.31	0.48	0.51	0.46	0.55	0.50	0.38	0.37	0.83	0	0	0	0	0	0	0	0
1-15E5	G1		1.74	1.71	0.79	0.30	0.25	1	0.99	0.31	0.97	0.30	0.37	0.96	1.19	2.49	1.09	1.09	0.33	0.68	1	1	1	1	1	1	1	1
1-15E5.2.1	G1		1.33	1.69	1.53	0.55	0.32	1	1.20	0.36	1.06	0.35	0.35	1.06	1.33	>3	1.23	1.14	0.34	0.65	1	1	1	1	1	1	1	1
3-4F10	G1		0.98	0.38	0.24	0.21	0.17	1	0.45	0.53	0.37	0.60	0.59	0.46	0.42	0.75	0.38	0.66	0.41	0.72	1	1	1	1	1	1	1	1
4-3D10	G3		1.23	1.19	0.79	0.33	0.25	1	0.90	0.33	0.92	0.33	0.44	0.74	0.95	2.31	1.06	0.92	0.37	0.91	1	1	1	1	1	1	1	1
4-4B11	G3		1.23	0.90	0.49	0.29	0.26	1	0.83	0.36	0.79	0.34	0.37	0.66	0.87	1.93	0.86	0.67	0.29	0.81	1	1	1	1	1	1	1	1
4-7E8	G3		0.00	-0.45	0.29	0.27	0.28	1	-1.46	-2.00	-1.46	-1.96	-1.94	-1.55	-1.28	-0.23	-1.23	-1.40	-1.97	-1.23	1	1	1	1	1	1	1	1
4-7H8	G3		1.45	1.29	0.54	0.31	0.27	1	0.74	0.26	0.66	0.20	0.31	0.63	0.84	2.04	0.87	0.66	0.28	0.58	1	1	1	1	1	1	1	1
4-10G6	G1		0.97	0.35	0.25	0.24	0.25	0	0.32	0.07	0.24	0.07	0.19	0.29	0.35	0.36	0.36	0.25	0.10	0.41	1	1	1	1	1	1	1	1
5-2G6	G1		0.58	0.42	0.31	0.25	0.25	1	0.47	0.07	0.27	0.06	0.18	0.29	0.40	1.05	0.38	0.20	0.09	0.38	1	1	1	1	1	1	1	1
5-2G8	G1		1.57	1.61	0.80	0.33	0.27	1	1.38	0.35	1.18	0.28	0.34	0.93	1.24	2.83	1.27	1.05	0.30	0.62	1	1	1	1	1	1	1	1
5-5E10	G1		1.74	1.59	0.57	0.29	0.26	1	1.33	0.31	1.28	0.30	0.34	0.93	1.33	2.74	1.24	1.03	0.31	0.59	1	1	1	1	1	1	1	1
5-9A7	G1		1.39	1.65	1.32	0.41	0.26	1	1.39	0.40	1.31	0.33	0.39	1.17	1.52	>3	1.51	1.42	0.37	0.66	1	1	1	1	1	1	1	1
5-9C7	G1		1.65	0.88	0.35	0.26	0.24	1	1.14	0.26	0.86	0.20	0.33	0.82	1.12	2.29	1.10	0.95	0.27	0.65	1	1	1	1	1	1	1	1
5-10G9	G1		0.97	0.77	0.36	0.26	0.26	1	0.25	0.03	0.02	0.03	0.16	0.18	0.19	0.13	0.17	0.05	0.06	0.40	1	1	1	1	1	1	1	1
6-7A4	G1		1.38	1.69	1.08	0.43	0.28	1	1.20	0.24	0.96	0.19	0.29	0.71	1.11	2.66	1.04	0.85	0.25	0.63	1	1	1	1	1	1	1	1
6-8-10E5	G1		-0.11	1.12	0.86	0.33	0.22	1	1.32	0.35	1.14	0.32	0.39	1.05	1.44	>3	1.44	1.41	0.38	0.52	1	1	1	1	1	1	1	1
7-1G9.1	G1		1.36	1.68	1.78	0.54	0.31	1	1.38	0.35	1.24	0.33	0.40	1.06	1.50	>3	1.46	1.32	0.36	0.68	1	1	1	1	1	1	1	1
7-7F12.1	G1		0.00	1.01	1.08	0.39	0.27	1	1.06	0.25	0.99	0.27	0.37	0.94	1.15	>3	1.27	1.06	0.31	0.39	1	1	1	1	1	1	1	1
7-9E2.1	G1		0.00	1.10	1.18	0.47	0.29	1	1.01	0.28	0.91	0.24	0.29	0.93	1.13	2.46	1.30	1.05	0.29	0.45	1	1	1	1	1	1	1	1

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☒ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☐ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**